

# LOCALIZATION OF ALU SEQUENCES THAT MATCH TO THE GENOMIC REGIONS THAT EXHIBITED EVIDENCE FOR LINKAGE TO MAJOR PSYCHOSIS

SZ - Alu clones from individuals affected with schizophrenia  
 BD - Alu clones from individuals affected with bipolar disorder  
 MD - major depression  
 CTRL - control samples

Sample Name (matched bp, %, chr band) number of ccgg sites	Homology length in bp; %	Chromosomal location	Evidence for linkage or association to schizophrenia or bipolar disorder
SZe-32m56	189, 99.5 %	6p22.3	Eckstein GN, Schwab SG, Maier W, Wildenauer DB. 1998. Searching for candidate genes for schizophrenia in chromosome 6p22.23: isolation of a BAC contig spanning 3.5 megabases. <i>Am J Med Genet</i> 81:530.
Sch37-9RR	160, 98.2 %	10p14	10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers D10S1423 and D10S582 were 3.4 ( $P = .0004$ ) and 3.2 ( $P = .0006$ ), respectively.
E-283m56SZ	190, 99.5%	10p14	Schwab et al. (1998a), <sup>1</sup> nonparametric LOD score of 3.2 ( $P = .0007$ ) at marker D10S1714(Schwab et al. 1998)
			(Straub et al. 1998)Straub et al. (1998) LOD score of 1.91 ( $P = .006$ ) at with markers D10S1426 and D10S674

<sup>1</sup> Schwab SG, Hallmayer J, Albus M, Lerer B, Hanses C, Kanyas K, Segman R, Borzman M, Dreikorn B, Lichterman D, Rietchel M, Truxler M, Maier W, Wildenauer DB. 1998. Further evidence for a susceptibility locus on chromosome 10p14-p11 in 72 families with Kanyargou M, Kasch L, Laxeter VK, Hwang J, Elango R, Bernardini DJ, Kimberland M, Babb R, Francomano CA, Wolyniec PS, et al., (1994). Report from the Maryland Epidemiology Schizophrenia Linkage Study: no evidence for linkage between schizophrenia and a number of candidate and other genomic regions using a complex dominant model. *Am J Med Genet*, 54:345-53 @ by nonparametric linkage analysis. *Am J Med Genet* 81:302-307.

Figure 1

SZr-37m56	183, 96.5 %	11q14.2	Mulcrone J, Whatley SA, Marchbanks R, Wildenauer D, Altmark D, Daoud H, Gur E, Ebstein RP, Lerer B. 1995. genetic linkage analysis of schizophrenia using chromosome 11q13-24 markers in Israeli pedigrees. Am J Med Genet 60:103-108.
E-318_m74_SZ	206, 97.7 %	22q12.2	22q11-13, Pulver et al. (1994a)(Pulver et al. 1994a; Pulver et al. 1994b; Pulver et al. 1994c) LOD score of 2.82 at marker locus IL2RB; ( $P = .009$ ) The implicated region is near the velocardiofacial syndrome (VCFS) deletion, Lasseter et al. 1995(Lasseter et al. 1995)  Polymoropoulos (Polymoropoulos et al. 1994)et al. 1994 Coon (Coon et al. 1994a; Coon et al. 1994b)et al. 1994a Stober (Stober et al. 2000)et al. 2000
E-305_m740_SZ E-221_m37_SZ E-267_m50_Ctrl E-288_m56_SZ E-289_m56_SZ E-297_m740_SZ E-295_m740_SZ E-294_m740_SZ E-293_m56_SZ E-286_m56_SZ E-252_m48_SZ E-244_m48_SZ E-130_m37_SZ SZm74-E-59 SZm74-E-58	191, 100 %	Yq12, Yq11.23, Yq11.223	Myles-Worsley(Myles-Worsley et al. 1999) et al. 1999 Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P, de la Chapelle A. 1988

Figure 1 Continued

SZm74-E-50 SZb_M37-1 SZb_M37-7 SZC_M37-5 SZC_M37-2 SZC_M37-26 SZC_M37-15 SZC_M37-7 SZC_M37-5 SZD_M37-14 SZRevCom48_E-33 SZRevCom48_E-39 SZm37-E-13_m37-7 Sch37-1 Sch37-6 Sch37-7 E-284m56SZ			191, 100 %	Yq12, Yq11.23, Yq11.223	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiuhonen J, Hakola P, de la Chapelle A. 1988
E-267_m50_Ctrl E-261_m50_Ctrl E-167m50Ctrl E-275m50Ctrl E-281m50Ctrl RevE-270m50Ctrl					
CONTROLS					
Ctrlm57-E-6	187; 99%	1q31.1		D1S2141 1q32-q41 Hovatta et al. (1998) (Hovatta et al. 1998) 1q32-41 Hovatta et al. (1999) (Hovatta et al. 1999) LOD score of 3.82 at marker D1S2891	
RevE-169m50Ctrl	179; 94.8%	1q31.1			

Figure 1 Continued

E-271m50Ctrl	155, 90.6 %	1q32.1	Schizophrenia Hovatta et al. (1998) (Hovatta et al. 1998) D1S2141 1q32-q41 Lod score 90% penetrance Lod score = 3.73
Ctrlm50E-49	185, 98 %	2q35	Event-related brain potential P3 Almasy et al. (1998)(Almasy and Blangero 1998) Between D2S425 and D2S434 2q33-q37 Bivariate quantitative linkage analysis Lod score = 3.28
Ctrlm57-E-3	191, 100 % or 189, 99.5 %	5q33.2 18q22.2	5q22-31 5q31 LOD score of 3.35 ( $P = .0002$ ) at marker D5S804 5q23.3 Straub et al. (1997) (Straub et al. 1997)  Marker D5S399 at 5q31  5q31.3-q35.1 was presented by Shink et al. [1998] <sup>2</sup> (Morissette et al. 1999)  Shink E, Morissette J, Rochette D, Bordeleau L, Plante M, Villeneuve A, Barden N. 1998. Bipolar affective disorder susceptibility loci on chromosomes 5 and 21: heterogeneity in a homogeneous population in Quebec.

Figure 1 Continued

Ctrlm57-E-5.	186, 97.4 %	13q14.11	13q14-32, Blouin et al. (1998)(Blouin et al. 1998) nonparametric LOD score of 4.18 ( $P = .00002$ ), near D13S174 on 13q32
E-166m50Ctrl	181, 100 %	18q23	Brzustowicz et al. (1999) Ewald et al. [1998] found increased haplotype sharing with distal markers at 18q23 in eight BPI patients from the Faroe Islands, in a region also suggested by Freimer et al. [1996].
E-279m50Ctrl	132, 94.7 %	18p11.23	18p11.2 and 18q12.1-q12.3 for BP and SZ, <sup>4</sup> Gershon et al. [1998] WCPG High density screen chromosome 18; average density 3.25 cM BP: 22 multiplex BP families [see (Berrettini et al. 1994)Berrettini et al. 1994] c ASM I: BPI, BPII, SA c ASM II: ASM I + RUP c Nonparametric analysis (ASPEX) c ASM I: highest peak on 18p11.2 (lod 4 2.32; $p$ 4 0.00054) c ASM II: smaller peak closer to 18ptel (lod 1.44; $p$ 4 0.005) c Smaller peak at 18q21 (lod $\square$ 1; not significant) c Confirmation previous evidence for linkage to 18p11.2
Ctrlm57-E-4.	193, 100 %	22q12.2	Confirmation previous evidence for linkage to 18p11.2 22q11-13, Pulver et al. (1994a)(Pulver et al. 1994a; Pulver et al. 1994b; Pulver et al. 1994c) LOD score of 2.82 at marker locus IL2RB same general region ( $P = .009$ ) The implicated region is near the velocardiofacial syndrome (VCFS) deletion, Lasseter et al. 1995(Lasseter et al. 1995) Polymeropoulos (Polymeropoulos et al. 1994)etal. 1994 Coon (Coon et al. 1994a; Coon et al. 1994b)etal. 1994a Stober (Stober et al. 2000)etal. 2000 Myles-Worsley(Myles-Worsley et al. 1999) et al. 1999

Figure 1 Continued

CtrIm57-6-E-1	155, 87.5 %	22q13.2	22q11-13 Baron(Baron 1990; Baron 1995) 1990, 1995; Baron et al (Baron et al. 1990). 1990; Risch (Risch 1990a; Risch 1990b) 1990a; Pauls (Pauls 1993) 1993; Spence (Spence et al. 1993) et al. 1993; Cloninger (Cloninger 1994) 1994; Lander and Kruglyak 1995(Lander and Kruglyak 1995); Owen and Craddock (Owen and Craddock 1996) 1996).
BD43-15	190, 98.7 %	21q21.3	C21q21-22 Susceptibility Locus for Bipolar and Unipolar Affective Disorders Repeated From Gurling [1998](Gurling 1998),
BD43-6	190; 99%	1q21.1	1q21-22 Brzustowicz et al. (2000)(Brzustowicz et al. 2000; Maziade et al. 2002) heterogeneity LOD score of 6.50 was found between markers D1S1653 and D1S1679, Shaw et al. 1998(Shaw et al. 1998)
RevE-77m43BD	191, 99.5 %	1p31.1	1q21 Dror et al. 1999(Dror et al. 1999) A potassium-channel gene (Hkca3/KCNN3) mapped to 1q21 - Austin et al. 1999). (- hKCa3/KCNN3) (Austin et al. 1999) Bipolar disorder Rice et al. (1997) D1S1648 1p31-p21 Sib-pair analysis MLOD2.5
BDD_M34-14BD (	187, 99 %	2p23.2).	Schizophrenia Blouin et al. (1998) (Blouin et al. 1998) D2S405 2p22.1 Nonparametric lod score NPI = 1.26 (p = 0.104)
E-79m43BD	186, 96.9 %	2q37.3	Event-related brain potential P3 Almasy et al. (1998)(Almasy and Blangero 1998) Between D2S425 and D2S434 2q33-q37 Bivariate quantitative linkage analysis Lod score = 3.28
E-78m43BD	192, 100 %	5q13.2;	5q11-13 Sherrington <sup>6</sup> et al. (1988)(Sherrington et al. 1988a; Sherrington

Figure 1 Continued

E-83m43BD	192, 100 % 192, 100 % 192, 100 %	5q22.2; 5q13.3; 16q23.1	<p>et al. 1988b), British and Icelandic pedigrees (a LOD score of 6.49, under a dominant model Maximum LOD score of 4.37 at locus D5S111 5q11-13 Silverman<sup>7</sup> et al. (1996)(Silverman et al. 1996) (Straub et al. 1997), (Bennett et al. 1997)</p> <p>Straub RE, MacLean CJ, O'Neill FA, Walsh D, Kendler KS. 1997. Support for a possible schizophrenia vulnerability locus in region 5q22-31 in Irish families. <i>Mol Psychiatry</i> 2:148-155.</p> <p>Bennett RL, Karayiorgou M, Sobin CA, Norwood TH, Kay MA. 1997. <i>Am J Hum Genet</i> 61:1450-1454.</p>
BDD_M34-19BD.	192, 100 %	10p14 or 10p13	<p>10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers D10S1423 and D10S582 were 3.4 (<math>P = .0004</math>) and 3.2 (<math>P = .0006</math>), respectively.</p> <p>Schwab et al. (1998a),<sup>8</sup> nonparametric LOD score of 3.2 (<math>P = .0007</math>) at marker D10S1714(Schwab et al. 1998)</p> <p>(Straub et al. 1998)Straub et al. (1998) LOD score of 1.91 (<math>P = .006</math>) at with markers D10S1426 and D10S674</p>
E-62m34BD	192, 100 %	10p14	<p>10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers D10S1423 and D10S582 were 3.4 (<math>P = .0004</math>) and 3.2 (<math>P = .0006</math>), respectively.</p> <p>Schwab et al. (1998a),<sup>9</sup> nonparametric LOD score of 3.2 (<math>P = .0007</math>) at marker D10S1714(Schwab et al. 1998)</p> <p>(Straub et al. 1998)Straub et al. (1998) LOD score of 1.91 (<math>P = .006</math>) at with markers D10S1426 and D10S674</p>

Figure 1 Continued

BDC- M34-10BD BDC- M34-1BD BD34-5 BD34-8 BD43-1 BD43-2	191, 100 %	Yq12, Yq11.23, Yq11.223	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P, de la Chapelle A. 1988
MDC- M39-2 MDD- M39-14 MD39-4 MD39-6 MD39-8 MD39-10 E-66m39MD	191, 100 %	Yq12, Yq11.23, Yq11.223	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P, de la Chapelle A. 1988

Figure 1 Continued

# GENES LOCATED IN THE CLOSE VICINITY TO THE CLONED *ALU* SEQUENCES

SZ - *Alu* clones from individuals affected with schizophrenia  
 BD - *Alu* clones from individuals affected with bipolar disorder  
 MD - major depression  
 CTRL - control samples

References in the brackets in the right hand side column indicate the papers in which implication of the detected genes in major psychosis was discussed.

Clone Name	Homology length in bp; %	Chromosoma location	Genes located in the close vicinity (within 100,000 bp)
E-285_m56_SZ	198; 99.5%	1q31.1	prostaglandin-endoperoxide synthase 2, PTGS2 {Das, 1998 #1; Smythies, 1997 #2; Geling, 1991 #3}
E-290_m56_SZ	189; 99.5%	1q31.1	ryanodine receptor 2 (cardiac), RYR2
E-149_m48_SZ	197; 99.5%	1q42.3	general transcription factor IIC, polypeptide 3, GTF3C3
E-154_m56_SZ	188; 99%	2q33.1	MSH3, mutS (E. coli) homolog 3
SZeRev_M37-6	187; 99%	5q14.1	CENPH, kinetochore protein CENP-H CFDP1, craniofacial development protein 1 (Goodman, 1996 #4) IL1A, interleukin 1, alpha CRHBP, corticotropin releasing hormone-binding protein
SZe-32m56	189, 99.5 %	6p22.3	Ataxin 1, SCA1 6 papers found on Schizophrenia. 3 items found on bipolar {Culjkovic, 2000 #100; Li, 1999 #101; Joo, 1999 #102; Pujana, 1997 #103; Morris-Rosendahl, 1997 #104; Wang, 1996 #105} {Morris-Rosendahl, 1997 #40; Fernandez Piqueras, 1995 #41}
E-311_m74_SZ	201, 100 %	8p21.3	docking protein 2, 56kD, DOK2
SZe-35m56	189, 99.5 %	8q24.23	hypothetical protein FLJ10901, FLJ10901
E-322_m74_SZ	192, 100%	7p22.3	C4S-2, chondroitin 4-O-sulfotransferase 2 EIF3S9, eukaryotic translation initiation factor 3
SZm74-E-60.	186, 99.5 %	8p23.1	hypothetical protein MGC16279

Figure 2

SZr-37m56	183, 96.5 %		11q14.2	embryonic ectoderm development, EED
E-310_m74_SZ	192, 100 %		14q21.3	ribosomal protein S29, RPS29 {Gentry, 2000 #49; Watanabe, 1996 #50} {Watanabe, 1994 #106}
E-313_m74_SZ	207, 97.7 %		15q26.3	MADS box transcription enhancer factor 2, MEF2A {Turner, 1997 #109}
E-258_m48_SZ	199, 98.6 %		17q21.33	distal-less homeobox 4, DLX4
E-16_m37_SZ	191, 99.5 %		17q23.2	tousled-like kinase 2, TLK2
E-319_m74_SZ	196, 100 %		18p11.32	Hypothetical protein FLJ23017, FLJ23017
E-315_m74_SZ	191, 100 %		19q12	highly expressed in cancer, rich in leucine, HEC
E-321_m74_SZ				ubiquinol-cytochrome c reductase, Rieske, UQCRCF1 {Johnston-Wilson, 2000 #53}
E-315_m74_SZ	191, 100 %		19p13.2	hypothetical protein FLJ14356, FLJ14356
E-315_m74_SZ				gonadotropin inducible transcription, GIOT-2
E-321_m74_SZ				Kruppel-type zinc finger (C2H2), ZK1
E-315_m74_SZ				hypothetical protein FLJ13659, FLJ13659
E-251_m48_SZ	198, 99.5 %		19p13.11	
E-2531_m48_SZ	189, 100 %		19p13.11	
E-2532_m48_SZ	188, 98.5 %		19p13.11	
E-325_m74_SZ	204, 96.7 %		19p13.11	hypothetical protein FLJ13659
E-178_m74_SZ	205, 98.1 %		19q13.12	zinc finger protein HZF10, ZNF345 Takase, 2001 #54; Ogura, 2001 #55; Sun, 2001 #56
E-246_m48_SZ	192, 100 %		20p12.3	hypothetical protein MGC4816, MGC4816
SZd M37-3	190, 100 %		20q13.2	LOC57167, similar to SALL1 (sal (Drosophila))-like
SZd M37-10	190, 97.9 %		20q13.2	LOC57167, similar to SALL1 (sal (Drosophila))-like
E-318_m74_SZ	206, 97.7 %		22q12.2	oncostatin M, OSM
E-305_m740_SZ	191, 100 %		Yq12, Yq11.23,	variable charge, Y chromosome, 2 protein, VCY2

Figure 2 Continued

E-221_m37_SZ E-288_m56_SZ E-289_m56_SZ E- 297_m740_SZ E- 295_m740_SZ E- 294_m740_SZ E-293_m56_SZ E-286_m56_SZ E-252_m48_SZ E-244_m48_SZ E-130_m37_SZ SZm74-E-59 SZm74-E-58 SZm74-E-50 SZb_M37-1 SZb_M37-7 SZC_M37-5 SZC_M37-2 SZC_M37-26 SZC_M37-15 SZC_M37-7 SZC_M37-5 SZD_M37-14 SZRevCom48_ E-33 SZRevCom48_ E-39 SZm37-E- 13 m37-7	Yq11.223	
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Figure 2 Continued

Sch37-1				
Sch37-6				
Sch37-7				
E-284m56SZ				variable charge, Y chromosome, 2 protein, VCY2
E-312_m74_SZ	172, 96.1 %		Yq12, Yq11.23, Yq11.223	
Ctrlm57-E-6	187; 99%		1q31.1	LOC51235, hypothetical protein
RevE-169m50Ctrl	179; 94.8%		1q31.1	PTGS2, prostaglandin-endoperoxide synthase 2 {Das, 1998 #1; Smythies, 1997 #2; Geling, 1991 #3}
				PIN1L, protein (peptidyl-prolyl cis/trans isomerase)
				long-chain fatty-acid-Coenzyme A ligase 3, FACL3
Ctrlm50E-49	185; 98%		2q35	
RevE-119m57Ctrl	192; 99.1%		3p22.2	SEC22C, vesicle trafficking protein, isoform a
	181; 97.4%		3p22.1	
Ctrlm57-E-3	191; 100% or 189, 99.5%		5q33.2 18q22.2	MRPL22, mitochondrial ribosomal protein L22 C5orf4, putative tumor suppressor PTGER4, prostaglandin E receptor 4 (subtype EP4) {Yeragani, 1987 #5}
Ctrl m50-26	73, 86.2 %		8q11.23	lysophospholipase I, LYPLA1
gDNA Ctrl	190, 99.5%		10p14	CUG triplet repeat, RNA-binding protein 2, CUGBP2
				GATA-binding protein 3, GATA3
gDNA Ctrl	187, 100 %		10q23.1	MGC4248, hypothetical protein MGC4248
				MGC16186, hypothetical protein MGC16186
				MGC11352, hypothetical protein MGC11352
				LHFP, lipoma HMGIC fusion partner
Ctrlm57-E-5	186, 97.4 %		13q14.11	PTPRM, protein tyrosine phosphatase, receptor type, mu (REF?? 1 items found on Schizoprenia. 4 items found on bipolar)
E-166m50Ctrl	181, 100 %		18q23	

Figure 2 Continued

Ctrlm57-E-2	163, 91 %	19q13.32	SULT2B1, sulfotransferase family, cytosolic, 2B, member
E-296 m57 Ctrl	179, 98.4 %	21q22.11	hormonally upregulated Neu-associated kinase, HUNK
Ctrlm57-E-4	193, 100 %	22q12.2	OSM, oncostatin M (Ref?? 2 papers found on bipolar WHAT??). LIF, leukemia inhibitory factor (cholinergic EPI64, EBP50-PDZ interactor of 64 kD SF3A1, splicing factor 3a, subunit 1, 120kD
Ctrlm57-6-E-1	155, 87.5 %	22q13.2	E1A binding protein p300, EP300
E-267_m50_Ctrl E-261_m50_Ctrl E-167m50Ctrl E-275m50Ctrl E-281m50Ctrl RevE- 270m50Ctrl	191, 100 %	Yq12, Yq11.23, Yq11.223	variable charge, Y chromosome, 2 protein, VCY2
BDd_M34- 14BD	187; 99%	2p23.2	BRE, brain and reproductive organ-expressed (TNFRSF1A. LRRFIP1, leucine rich repeat (in FLII) interacting
BD43-10	192; 99.1%	3p22.2	SEC22C, vesicle trafficking protein, isoform a
E-74m43BD	181; 97.4%	3p22.1	SHC3, neuronal Shc
BDc_M34-4BD	195, 99.5 %	9q22.2	FOLR1, folate receptor 1 precursor
BDc_M34-3BD	191, 100 % or 191, 100 %	11q11 11q13.4	SKD3, suppressor of potassium transport defect 3 INPPL1, inositol polyphosphate phosphatase-like 1 FOLR2, folate receptor 2 precursor . ARIX, aristalless (Drosophila) homeobox
BD43-8	178, 100 %	11q22.3	nuclear protein, ataxia-telangiectasia locus, NPAT {Lange, 1989 #114; Weeks, 1989 #115}
E-72m43BD	160, 100 %	16q13	CNGB1, cyclic nucleotide gated channel beta 1
BD43-14	191, 100 %	16q24.2	hypothetical protein FLJ23497

Figure 2 Continued

E-71m39MD	147, 92 %	15q26.1	PRC1, protein regulator of cytokinesis 1
BDd_M43-19BD.	201, 100 %	19p13.11	KCNN1, potassium intermediate/small conductance (REF ?? 1 items found on Schizophrenia. 2 items found on bipolar. SLC5A5, solute carrier family 5 (sodium iodide.
BDC- M34-10BD	191, 100 %	Yq12, Yq11.23, Yq11.223	IL12RB1, interleukin 12 receptor, beta 1 (41 papers found. on interleukin receptor & schizophrenia; 5 items found. on interleukin receptor & bipolar. variable charge, Y chromosome, 2 protein, VCY2
BDC- M34-1BD			
BD34-5			
BD34-8			
BD43-1			
BD43-2			
MD39-4			
MD39-6			
MD39-8			
MD39-10			
MDC- M39-2			
MDD- M39-14 (190, 100)			
E-66m39MD			

Figure 2 Continued

Cloned *Alu* sequences

SZ- from individuals affected with schizophrenia

CNTR- from control samples

BD - from individuals affected with bipolar disorder

MD - from individuals affected with major depression

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> E-130_m37_SZ
CTGATTACGCCAAGCTCTAATACGACTCACTACTATAGGAAAGCTCGGTACCAAGCATGCTTGCGAGACGCGTTACGT
ATCGGATCCAGAAATTCGTGATTGGAGGGTGTTCGACAAATCTCAGCTCACCGAAACCTCCGGCTCACAGGTCAAG
TGATTCCTCTGCCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCAATTTGCCATGATACCTGGCTAATTTGTATTTT
AGTAGAGACCAAGGATTCATGTTGATAAGGTGGTTCCTTGAACCTCTGACCTCAGATGATCCATCTGATTTGGCC
TCCCAAACCTGCTGGGAGTACAGGCAATCTGAATTCGTGACAAAGCTTCTCGAGCCTAGGCTAGCTAGACCAACA
CGTGTGGGGCCCGAGCTCGGGCCGCTGTATTCATAGTGTACCTAAATGGCCGACAAATTCACCTGGCCGTCGT
TTTACAACGTCGTGACTGGGAAACCTCGCGTTACCCAACTTAATCGCCTTGCGAGCACATCCCCCTTTCCACGCT
GGCGTAATAGACGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGGCAAGCCTG

> E-140_m48_SZ
CTATCCCATGATTACGCCAAGCTCTAATACGACTCACTACTATAGGAAAGCTCGGTACCAAGCATGCTGCAGACGCG
TTACGATATCGGATCCAGAAATTCGTGATTGCCTGTACTCCAGCAGTTTGGGAGGCTGAGGTAGGTGGATCACGAG
GTCAGGAGTTCTAGATCAGCCTGGCCAAACAGGGTGAACCATGTCTCTACTAAATAACAAAATAGTCAGGCG
TGGTGGTGGCACCTGTAAATCCAGTTACTTTGGGAGGCTGAGGCAGGAGAAATTTCTTGAACCTGGAGGCAGAGG
TTGCAGTCAGCCGAGATTGTGCAAAACACCTCCAATCTGAATTCGTGACAAAGCTTCTCGAGCCTAGGCTAGCTCT
AGACCACAGCTGTGGGGCCCGAGCTCGGGCCGCTGTATTCATAGTGTACCTAAATGGCCGACAAATTCACCT
GGCCGTCGTTTACAAACGTCGTGACTGGGAAACCTGGCGTTACCCAACTTAATCGCCTTGCGAGCACATCCCCCTT
TCGCCAGCTGGCGTAATAGCGAAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGGCAGCCTGAATGGCGAATG
GAAATGTAA

> E-150_m48_SZ
CTATGACCATGATTACGCCAAGCTCTAATACGACTCACTACTATAGGAAAGCTCGGTACCAAGCATGCTGCAGACGC
GTTACGATATCGGATCCAGAAATTCGTGATTGCCTGTACTCCAGCAGTTTGGGAGGCTGAGGTAGGTGGATCATCTG

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Figure 3

AGGTCAGGAGTTCAGAACCACCTTATCAACATGAAGAATCTGTGCTCTACTAAAGTACAAATTAGCCAGGT  
 ATCATGGCAAAATGCTTGTCTACTAGCTACTCAGAAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGCGGAG  
 GTTTCGGTGAGCTGAGATTGTGCAACACCCCTCCAAATCTGAATTCGTGACAAAGCTTCTCGAGCCTAGGCTAGCTC  
 TAGACCACACGTGTGGGGCCGAGCTCGCGCCGCTGTATTCTATAGTGCACCTAAATGGCCGACAAATTCACCT  
 GGCCGTGTTTTACAAACGTGCTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCT  
 TTCGCCAGCTGGCGTAATAGCGAAGAGGGCCGACCGATCGCCCTTCCAAACAGTTGGCAGCCTGAATGGCGA

> E-154\_m56\_SZ  
 ATGATTACGCCAAGCTCTAATAACAACCTACTATGCGCAATGGTGGCAACCTCGCATGCTGCATACGCGTTACGTA  
 TCGGATCCAGAAATTCGTGATTGGAGGTGTTTGCACAATCTCAGCTCACTGCAACCTCCACCTCCAGGCTCAATG  
 ATCTCCACCTCAACTCCCCGAGTAACCTGGACCAACAGGTGCAATGCCAGCATGCCAGCTAATTTTGTATTTT  
 CTGTTGAGATGGGTTTTGCCATGTTGCCAGGCAAGTCTCGAACTGCTGGGCTCAAGTGATCTCTGCTGCCCTCCAC  
 CTCACAACTGCTGGGAGTACAGGCAATCTGAATTCGTGACAAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCAC  
 ACGTGTGGGGCCGAGCTCGCGCCGCTGTATTCTATAGTGTCACTAAATGGCCGCAACATTCACCTGAGCCGTG  
 TTTTACAACGTGCTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAG  
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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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4> E-319\_m74\_SZ

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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0> E-279m50Chl

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GAAAT

2> E-281m50Chl

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2> E-283m56SZ

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2> E-284m56SZ

Figure 3 Continued

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7> E-61m34BD

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2> E-62m34BD

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2> E-63m34BD

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Figure 3 Continued

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2> E-66m39MD  
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Figure 3 Continued

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3> E-74m43BD  
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> E-77m43BD  
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Figure 3 Continued

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> E-78m43BD

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Figure 3 Continued

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> E-283m56SZ

Figure 3 Continued

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>> E-63m34BD

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>> E-68m39MD

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Figure 3 Continued

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Figure 3 Continued

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 Sorry, no matches found

S> RevE-119m57Ctrl

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2> RevE-270m50Ctrl

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S> RevE-169m50Ctrl

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Figure 3 Continued

3> RevE-77m43BD  
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2> PK1601mM-13\_m37-7+++  
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2> PK1601mM-11\_m37-5+++  
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5> PK1601\_mM-1\_m57-6-----  
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3> PK1601mM-60+++  
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2> PK1601mM-59+++  
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2> PK1601mM-58+++

Figure 3 Continued

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3[]> PK1601mM-57+++  
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2> Pk1601mM-54+++  
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2> pk1601mM-53+++  
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5> pk1601mM-52+++  
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Figure 3 Continued

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 []10> pk1601mM-37+++

Figure 3 Continued

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9> pk1601\_mM-35+++  
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5> pk1601\_mM-32+++  
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7> pk1401\_mM-24+++  
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4> pk1401\_mM-23+++  
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Figure 3 Continued

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7> pk1401\_mM-21++  
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2>pk1401 mM-18+++

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2>pk1401 mM-17+++

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4> pkl401\_mM-16+tt

Figure 3 Continued

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2> pk1401\_mM-14+++

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2> pk1401\_mM-8-----

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pk1401\_mM-6-----

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PK1401\_mM-4-----

Figure 3 Continued

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pk1401\_mM-2  
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pk1401\_mM-2-----  
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SZb\_m37-10+++  
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SZb\_m37-9+1+1+

Figure 3 Continued

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SZb m37-7+++  
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Figure 3 Continued



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pk0301\_M39-14-----BD-----  
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PK0301\_M37-14+++

Figure 3 Continued

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PK0301\_M37-11+++

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RevCompSZB\_M37-6+++

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RevCompPK1401\_mM-17+++

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RevCompPK1601mM-33+++

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CUTPK1601\_mM-1\_m57-6-----

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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Figure 3 Continued

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 GGCAAGCCGAATTCGCAGATATCCATCACACTGGGCGCGCTCGAGCATGCATCTAGAGGGCCCAATTCGCCCT  
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Figure 3 Continued

>PK39-3withM13R  
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CAAGCCGAATCTGCAGATATCCATCACACTGGCGGCTCGAGCATGCACTAGAGGGCCCAATTCGCCCTAT  
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Figure 3 Continued

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Figure 3 Continued

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**>BD43-1 with M13R**

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**>BD43-2withM13R**

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TGTGTGATAAGGTGGTCTTGAACCTCTGACCTCAGATGATCCATCTGATTTGGCCTCCAAACTGCTGGGAGTACA  
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**>BD43-6withM13R**

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GCGCCCTAGCGCCCG

4>BD43-8

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GGGCTGCTTGAATCTTGGCTCAAGAGATCCGCTGCTTTGGCCTCTCAAACTGCTGGAGTACAGGCAAGCCG  
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Figure 3 Continued

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AGCCTGAATGGCGAATGGACGCGCCTGTAGCGGCGCATTAAGCGGCGGGTGTGTGGTTACGCGCAGCGTGAC  
C

4>BD43-8(2)withM13R BD43-8 (178, 100, 11q22.3)  
GGAGGGTGTTTGACAAATCTTGGCTCACTGCAACCTCCACCTCGCAGTTCAGCAATTCCTGTGCCTTAGCCTCCT  
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C

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CATGTTGCCAGGCTGATCTCGAACCCCTGACCTCAACTGATCCACCCACCTCGCCCTTCCAAACTGCTGGGAGTA  
CAGGCAAGCCGAAATCTGCAGATATCCATCACACTGGGCGCGCTCGAGCATGCATCTAGAGGGCCCAATTCGCC  
CTATAGTAGTCGTATTACAATTCACTGGCGCTGTTTACAAACGTCGTGACTGGGAAACCCCTGGCGTTACCCAA  
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>BD43-14 (191, 100, 16q24.2) withM13R

Figure 3 Continued

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GGCAAGCCGAATCTGCAGATATCCATCACTGGCGCGCTCGAGCATGCACTCTAGAGGGGCCCAATTGCCCCCT  
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Figure 3 Continued

